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EXAMINER

SULLIVAN, DANIEL M

ART UNIT	PAPER NUMBER
1636	

DATE MAILED: 09/27/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

09/997,425

Applicant(s)

EDINGER ET AL.

Examiner

Daniel M Sullivan

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-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 14 July 2004.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-49 is/are pending in the application.
- 4a) Of the above claim(s) 1-4, 15-38, 40, 41 and 43-49 is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 5-14, 39 and 42 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☒ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. _____.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date 3/7/02.
- 4) ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____.
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☒ Other: 6 pages sequence alignments.

DETAILED ACTION

This is the First Office Action on the Merits of the Application filed 29 November 2001, which claims benefit of US patent application 10/035,568 filed 22 October 2001, and US Provisional applications 60/242,485 filed 23 October 2000, 60/263,339 filed 2 January 2001 and 60/264,850 filed 29 January 2001. The preliminary amendment filed 8 October 2002 has been entered. Claims 1-49, as originally filed, are pending in the application.

Election/Restrictions

Applicant's election with traverse of Group II (claims 5-14, 39 and 42) and SEQ ID NO: 51 in the reply filed on 14 July 2004 is acknowledged. The traversal is on the ground(s) that examination of all of the Groups in a single application would not impose an undue burden on the Office.

With regard to the subject matter of Groups I-X, this is not found persuasive for the following reasons:

Searching the polypeptide of Group I with the polynucleotide of Group II would impose a serious burden because the subject matter embraced by the groups is not coextensive. First, the Inventions of Groups I and II are separately classified, which is *prima facie* evidence of the additional burden imposed by searching both inventions together. Furthermore, a search of the nucleic acid and polypeptide sequences must be performed in separate databases and a determination that the nucleic acid of Group II is patentable cannot be taken as evidence for the patentability of the polypeptide of Group I, and *vice versa*. A search for the polypeptide of Group I would not reasonably embrace the subject matter of Group II because the art might disclose the

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polypeptide without disclosing a nucleic acid sequence encoding the polypeptide. Given the degeneracy of the genetic code and the fact that the claims of Group II recite specific embodiments of nucleic acids encoding the polypeptides, rather than being generic to any nucleic acid encoding the polypeptide, a disclosure of a polypeptide according to Group I does not render obvious the full scope of Group II (*i.e.*, the specific nucleic acid sequences recited in the claim). Likewise, a search of the art for the polynucleotide of Group II would not reasonably embrace the full scope of the subject matter of Group I because the art might disclose the polypeptide sequence determined by direct amino acid sequencing, without a disclosure of the nucleic acid sequence. Therefore, a determination that either Group is free of the art does not adequately support patentability of the other Group and an additional search is required to establish patentability.

Likewise, searching the antibody of Group III with the polypeptide of Group I or nucleic acid of Group II would impose a serious burden on the office. Again, the Inventions are separately classified, which is *prima facie* evidence of the additional burden imposed by searching both inventions together. Furthermore, a determination that the antibody of Group III is free of the art does not adequately support patentability of the claimed protein or nucleic acids and *vice versa*. Because the art might disclose the protein or nucleic acid independently of an antibody that binds to the polypeptide or polypeptide encoded by the nucleic acid, and because an antibody that binds to the polypeptide of Invention I or encoded by the nucleic acid of Invention II might be disclosed in the absence of a disclosed polypeptide or nucleic acid sequence, determining patentability of Group III requires additional searching beyond what is

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required for Group I or Group II, and determining patentability of Group I and Group II requires searching beyond a search for the subject matter of Group III.

At least for the reasons set forth above regarding the products, a method of making or using the product of Group I *versus* the product of Group II *versus* the product of Group III cannot be searched coextensively. Therefore, searching the methods of making and using each of the distinct products in a single application imposes a serious burden on the Office.

Finally, although the Office has acknowledged that in the event a product claim is deemed allowable determining patentability of the methods of making and using the product does not impose an undue burden, in the instant case the elected product is not patentable. Therefore, a determination of whether each method of making and using the product is patentable over the art is based upon the particulars of the method and not on the product made by or used in the method. As a search of a method of determining the amount or presence of a nucleic acid according to Group V would not reasonably encompass a method of treating or preventing a pathology according to the method of Group X and *vice versa*, examining the methods together in a single application imposes a serious additional burden. However, as stated in the restriction requirement, where applicant elects claims directed to the product, and a product claim is subsequently found allowable, withdrawn process claims that depend from or otherwise include all the limitations of the allowable product claim will be rejoined in accordance with the provisions of MPEP § 821.04.

Applicant additionally argues that the antibodies of Group III are not independent of the polypeptide of Group I. This was acknowledged in the restriction requirement, which states:

“The polypeptide of Invention I is related to the antibody of Invention III by virtue of binding affinity. Although the polypeptides and antibodies are related

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since the antibody binds to the polypeptide and can be raised by immunization with the polypeptide, they are distinct inventions because they are physically and functionally distinct chemical entities, and the antibody can be made obtained by another and materially different process, such as by purification from a natural source or by immunization with chemically synthesized peptides. Further, the polypeptide may be used for processes other than the production of the antibody, such as a standard in an assay for the presence of the protein.” (emphasis added).

Thus, the basis of the restriction requirement is that the Groups are directed to “distinct” inventions. “The law has long been established that dependent inventions (frequently termed related inventions) such as used for illustration above may be properly divided if they are, in fact, ‘distinct’ inventions, even though dependent.” MPEP 802.01.

Applicant’s arguments have been fully considered but are not deemed persuasive either individually or as a whole; therefore, the requirement is still deemed proper and is therefore made FINAL.

However, with regard to the nucleic acid encoding a polypeptide set forth as SEQ ID NO: 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54 and 56, Applicant’s assertion that the nucleic acids are distinct species of the same invention is found persuasive. Currently, claim 5 is generic. Upon the allowance of a generic claim, applicant will be entitled to consideration of claims to additional species which are written in dependent form or otherwise include all the limitations of an allowed generic claim as provided by 37 CFR 1.141. If claims are added after the election, applicant must indicate which are readable upon the elected species. MPEP § 809.02(a).

Claims 1-4, 15-38, 40, 41 and 43-49 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention, and nucleic acids limited to encoding polypeptides comprising SEQ ID NO: 2, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44,

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46, 48, 50, 54 or 56, are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected species, there being no allowable generic or linking claim. Claims 5-14, 39 and 42 and a nucleic acid encoding SEQ ID NO: 52 are presently under consideration.

Priority

Applicant has not complied with one or more conditions for receiving the benefit of an earlier filing date under 35 U.S.C. 119(e) and 120 as follows:

The later-filed application must be an application for a patent for an invention which is also disclosed in the prior application (the parent or original nonprovisional application or provisional application); the disclosure of the invention in the parent application and in the later-filed application must be sufficient to comply with the requirements of the first paragraph of 35 U.S.C. 112. See *Transco Products, Inc. v. Performance Contracting, Inc.*, 38 F.3d 551, 32 USPQ2d 1077 (Fed. Cir. 1994).

In the instant case, the priority applications do not disclose a nucleic acid encoding the elected SEQ ID NO: 52. Thus, there is neither explicit nor implicit support for the elected species in the parent applications sufficient to comply with the requirements of the first paragraph of 35 U.S.C. 112. The claims will be afforded an effective filing date of 29 November 2001 (*i.e.*, the filing date of the present application).

Specification

The disclosure is objected to because of the following informalities:

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The priority claim, which was amended on 8 October 2002 to include the serial number of the '568 application, does not indicate the relationship of the non-provisional application to the instant application. It would seem that the present application is a continuation-in-part of the '568 application and the first line of the specification should be amended accordingly.

The title of the invention is not descriptive. A new title is required that is clearly indicative of the invention to which the claims are directed.

The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code (*e.g.*, at page 13, line 19 and page 15, line 7). Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01.

The disclosure contains a number of typographical errors (*e.g.*, page 38, line 6 reads, "60% percent" and there are boxes where there should presumably be Greek letters at page 113, line 31). Applicant is urged to carefully review the disclosure and correct any typographical errors.

Appropriate correction is required.

Claim Construction

The following is a description of how certain claim limitations are construed by the Examiner in light of the teachings of the specification.

The limitation "mature form", appearing in claim 5, is defined in the paragraph bridging pages 39-40 of the specification as "the product of a naturally occurring polypeptide or precursor

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form or proprotein.” Although the specification provides some examples of how a “mature form” of a polypeptide might be produced, these are explicitly identified as “nonlimiting”. Therefore, the broadest reasonable interpretation of “mature form” according to the description provided encompasses a product of a naturally occurring polypeptide produced by any means. For example, the claim reads on a nucleic acid encoding any degradation product of the naturally occurring polypeptide.

The limitation “variant”, appearing in claims 5-7, is understood based on the discussion in the first paragraph on page 38 as encompassing a protein “any of whose residues may be changed from the corresponding residue shown in Table 1B while still encoding a protein that maintains its endozepine-related protein precursor-like activities and physiological functions, or a functional fragment thereof. In the mutant or variant protein, up to about 60% percent [sic] of the residues may be so changed.”

The limitation “stringent conditions”, appearing in claim 10, is understood according to the discussion in the first full paragraph on page 46 to encompass hybridization under conditions of any stringency known in the art (*i.e.*, very low, low, high, *etc.*).

Claim 11, part (a) recites “a first nucleotide sequence comprising a coding sequence differing by one or more nucleotide sequences from a coding sequence...” (emphasis added). Given the plural “sequences” the claim is understood to require a difference in two or more contiguous nucleotides.

Claim Objections

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Claim 10 objected to because of the following informalities: The preposition “of” should be inserted between “consisting” and “SEQ ID NO” in lines 2-3 of the claim. Appropriate correction is required.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 5-14, 39 and 42 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a specific and substantial asserted utility or a well-established utility.

The pending claims have been reviewed in light of the Utility Examination Guidelines and Guidelines for Examination of Patent Applications under 35 U.S.C. §112, first paragraph, “Written Description” Requirement, Federal Register, Vol. 66, No. 4, pages 1092-1111, Friday, January 5, 2001

The Examiner is using the following definitions in evaluating the claims for utility.

“Specific”-A utility that is *specific* to the subject matter claimed. This contrasts with a *general* utility that would be applicable to the broad class of the invention.

“Substantial”-A utility that defines a “real world” use. Utilities that require or constitute carrying out further research to identify or reasonably confirm a “real world” context of use are not substantial utilities.

“Credible”- Credibility is assessed for the perspective of one of ordinary skill in the art in view of the disclosure and any other evidence of record that is probative of the applicant’s assertions. That is, the assertion is an inherently unbelievable undertaking or involves implausible scientific principles.

“Well-established”-a specific, substantial and credible utility which is well known, immediately apparent, or implied by the specification’s disclosure of the properties of a material alone or taken with the knowledge of one skilled in the art.

The claimed subject matter is not supported by either a specific or substantial asserted utility because the disclosed utilities are generally applicable to a broad class of molecules and the specification fails to set forth the unique properties of the claimed invention such that the skilled artisan would recognize a specific real-world utility therefor.

The claims are directed to an isolated nucleic acid encoding a mature form of a polypeptide set forth as SEQ ID NO: 52, identified as NOV2q, and variants thereof. Claims are also directed to vectors and host cells and pharmaceutical compositions comprising said nucleic acids.

In the first paragraph on page 31, the specification teaches that the NOV2a and its variants, such as the claimed NOV2q, are “endozepine-related protein precursor-like proteins” and novel members of the endozepine-related protein precursor-like protein family, and asserts utility “in potential therapeutic applications implicated in various pathologies and disorders described and other pathologies and disorders related to aberrant function or aberrant expression of these endozepine-related protein precursor-like proteins.” The specification variously teaches that the claimed invention can be used to make a transgenic animal (page 77-79), to make a pharmaceutical composition (page 80-83), can be applied as a therapeutic in gene therapy applications (page 83, lines 15-16), can be used to develop various pharmaceuticals (page 83-89 and 99), can be used in chromosome mapping (page 90), can be used to identify individuals from a minute biological sample (page 92) and can be used in predictive medicine to diagnose and treat a wide variety of conditions (page 93 and 103). However, none of the teachings with regard to the asserted utilities are specific to the claimed invention. Instead, they are generic recitations of what essentially any nucleic acid might be used for, or are based on unsubstantiated properties

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of the nucleic acid. The specification provides no description of the uniquely useful properties of a transgenic animal made with the claimed invention, discloses no specific population of individuals that can be identified using the claimed invention and provides no specific teaching as to which diseases within the broadly divergent set of conditions contemplated might actually be diagnosed or treated using the invention or reagents developed therewith. Thus, the asserted utilities are not specific.

Furthermore, even if a specific utility were among those set forth in the specification, identifying or reasonably confirming a “real world” context of use for the claimed nucleic acid would clearly require additional experimentation. The only basis for the utilities asserted for the claimed invention, beyond its being a nucleic acid encoding a protein, is the structural similarity of the NOV2q polypeptide encoded by the claimed nucleic acid to a protein known in the art as “membrane-associated diazepam binding inhibitor” or MA-DBI (*i.e.*, approximately 83% identical based on the BLAST results for NOV2a provided on page 14-15); however, on page 31, line 34, the specification teaches that the function of MA-DBI is unknown. It is noted that, although the table on page 15 also indicates a higher degree of homology with polypeptides disclosed in a PCT application which names inventors in common with the instant application (*i.e.*, WO0078802) and a “hypothetical 31.5kDa protein”, the asserted function for the polypeptide disclosed in the PCT application is also based on similarity to MA-DBI and the function of the hypothetical protein is unknown.

In the third paragraph on page 31, NOV2q is also assigned to the Acyl-CoA-binding protein family and the specification provides that this family includes, in addition to MA-DBI,

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the mouse endozepine-like peptide and human DRS-1, another protein of unknown function (page 31, lines 35-36). The specification identifies a region of NOV2q having homology to acyl-CoA-binding protein/diazepam binding inhibitor (DBI; Table 12E, page 15), a small protein having a number of physiological and biochemical functions (pages 32-37). However, Todaro *et al.* (1991) *Neuropharmacology* 30: 1373-1380 teaches that although MA-DBI has significant homology with the acyl-CoA-binding domain of DBI, the region of DBI that gives rise to the biologically active octadecaneuropeptide has low homology (see especially the second column on page 1375). Therefore, although MA-DBI is likely to bind acyl-CoA, it is unlikely to have the same neuromodulatory effects as DBI, and Todaro *et al.* teach that, as of 1991, the function of MA-DBI was unknown (paragraph bridging pages 1375-1376), which is acknowledged in the instant specification to still be the case as of the effective filing date of the application (*Id.*). Thus, the function of the claimed invention is based on similarity to proteins whose function is acknowledged to be unknown.

Furthermore, even if the function of MA-DBI were known, the art generally acknowledges that function cannot be predicted based solely on structural similarity to a protein found in the sequence databases. For example, Skolnick *et al.* (2000) *Trends Biotechnol.* 18:34-39 teach that knowing the protein structure by itself is insufficient to annotate a number of functional classes, and is also insufficient for annotating specific details of protein function (see Box 2, page 36). Similarly, Bork (2000) *Genome Res.* 10:398-400 teaches that the error rate of functional annotations in the sequence database is considerable, making it even more difficult to infer correct function from a structural comparison of a new sequence with a sequence database (see especially page 399). Smith *et al.* (1997) *Nature Biotechnol.* 15:1222-1223 teaches,

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“[t]ypical database searching methods are valuable for finding evolutionarily related proteins, but if there are only about 1000 major superfamilies in nature, then most homologs must have different molecular and cellular functions” (second column on page 132). These teachings demonstrate the unpredictability of assigning protein function based on structure alone.

As the functional characteristics of the claimed nucleic acid are unknown and there is no established link between the claimed invention and any particular disease state or specific identifiable population, it would clearly require substantial experimentation to reasonably identify or confirm a “real world” context of use for the claimed invention. Thus, the asserted utilities are not substantial.

Finally, as the art also fails to teach a specific useful characteristic of the claimed invention, or any closely related nucleic acid, such that a specific and substantial utility for the claimed invention would be readily apparent, the skilled artisan would not recognize a patentable utility which is well known, immediately apparent, or implied by the specification’s disclosure of the properties of a material alone or taken with the knowledge of one skilled in the art.

Applicant should explicitly identify a specific and substantial credible utility for the claimed invention and establish a probative relation between any evidence of record and the originally disclosed properties of the claimed invention.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

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Claims 5-14, 39 and 42 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Vas-Cath Inc. v. Mahurkar, 19USPQ2d 1111, clearly states that “applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of *the invention*. The invention is, for purposes of the ‘written description’ inquiry, *whatever is now claimed*.” (See page 1117.) The specification does not “clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed.” (See *Vas-Cath* at page 1116).

In the instant case, claims are directed to a nucleic acid encoding variants of the polypeptide sequence set forth as SEQ ID NO: 52, wherein a variant is a polypeptide whose residues may be changed from the disclosed sequence while still encoding a protein that maintains its endozepine-related protein precursor-like activities and physiological functions, or a functional fragment thereof (*Id.*). In claims 6 and 7, the variant is limited to being a naturally occurring allelic nucleic acid variant or a naturally occurring polypeptide variant. Thus, the variant of the claims is generic to a structurally divergent set of nucleic acid molecules encoding any polypeptide having up to about 60% of the amino acids changed relative to the disclosed amino acid sequence, or fragment thereof, and retaining some unspecified endozepine-related protein precursor-like activity.

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The Guidelines for Written Description state: “when there is substantial variation within the genus, one must describe a sufficient variety of species to reflect the variation within the genus” (Federal Register, Vol. 66, No. 4, Column 3, page 1106). “The written description requirement for a claimed genus may be satisfied through sufficient description of a representative number of species by actual reduction to practice..., reduction to drawings..., or by disclosure of relevant, identifying characteristics, i.e., structure or other physical and/or chemical properties, by functional characteristics coupled with a known or disclosed correlation between function and structure, or by a combination of such identifying characteristics, sufficient to show the applicant was in possession of the claimed genus” (MPEP §2163(3)(a)(ii)).

In the instant case, although several naturally occurring sequence variants of the claimed invention are disclosed in the application (*i.e.*, nucleic acids encoding SEQ ID NO: 2, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 54 and 56) the specification fails to disclose which of the sequence variants actually have endozepine-related protein precursor-like activities and physiological function, which activities and functions are not specifically disclosed in the application (*Id.*). Thus, it is not clear how many of the disclosed species are actually representative of the claimed genus of “variants”. Furthermore, as stated in MPEP 2163(I)(A), “A biomolecule sequence described only by a functional characteristic, without any known or disclosed correlation between that function and the structure of the sequence, normally is not a sufficient identifying characteristic for written description purposes, even when accompanied by a method of obtaining the claimed sequence.” In the instant case, the disclosure provides only a vague unsubstantiated assertion as to the function of the claimed nucleic acid and no disclosure at all of important structural determinants for the endozepine-related protein precursor-like

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activities and physiological functions. Thus, the skilled artisan could not possibly envision the structural determinants of endozepine-related protein precursor-like activities and physiological functions such that one would acknowledge Applicant was in possession of the claimed variants at the time of filing.

With regard to naturally occurring allelic variants, the disclosure provides no written description for any naturally occurring variants of NOV2q beyond those explicitly disclosed in the application. The general knowledge in the art concerning alleles does not provide any indication of how the structure of one allele is representative of unknown alleles. The nature of alleles is that they are variant structures, and in the present state of the art the structure of one does not provide guidance to the structure of others. One of skill in the art would conclude that Applicant was not in possession of the claimed genus because a description of any given member of the genus, or even multiple species within the genus, provides no support for the structure of any species within the genus that is not disclosed.

Claims 5-14, 39 and 42 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

First, since the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

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Furthermore, even if Applicant could identify a specific and substantial asserted utility, using the claimed invention for any of the purposes set forth in the specification would require undue experimentation.

There are many factors to be considered when determining whether there is sufficient evidence to support a determination that a disclosure does not satisfy the enablement requirement and whether any necessary experimentation is "undue." These factors include, but are not limited to: (a) the nature of the invention; (b) the breadth of the claims; (c) the state of the prior art; (d) the amount of direction provided by the inventor; (e) the existence of working examples; (f) the relative skill of those in the art; (g) whether the quantity of experimentation needed to make or use the invention based on the content of the disclosure is "undue"; and (h) the level of predictability in the art (MPEP 2164.01 (a)).

Nature of the invention and Breadth of the claims: The claims are directed to an isolated nucleic acid encoding a mature form of a polypeptide set forth as SEQ ID NO: 52, identified as NOV2q, and variants thereof. Claims are also directed to vectors and host cells and pharmaceutical compositions comprising said nucleic acids. As discussed above, the claims broadly encompass nucleic acids encoding polypeptides of substantial structural diversity.

State of the prior art and level of predictability in the art: As described above, the closest art discloses a nucleic acid encoding a polypeptide that is approximately 85% identical to the instant SEQ ID NO: 52. However, the art fails to teach any specific and substantial useful property for the nucleic acid disclosed therein. In fact, the art teaches that the function of the related protein is unknown (Todaro *et al.*; *supra*) and this acknowledged in the instant

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specification. Thus, the art does not suggest any particular useful property shared by any protein having 85% identity with the protein disclosed therein or nucleic acid encoding the protein.

Furthermore, art does not suggest any therapeutic or diagnostic utility for an MA-DBI, let alone a nucleic acid encoding a protein having limited structural similarity to an MA-DBI. Thus, the skilled artisan is fully dependent upon the teachings of the instant application to provide a written description of the manner and process of using the invention in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, use the same without undue experimentation

Amount of direction provided by the inventor and existence of working examples: As described above, the specification variously teaches that the claimed invention can be used to make a transgenic animal, to make a pharmaceutical composition, can be applied as a therapeutic in gene therapy applications, can be used to develop various pharmaceuticals and can be used in predictive medicine to diagnose and treat a wide variety of conditions. However, the specification fails to provide information fundamental to practicing any of the asserted utilities. Although, the specification provides detailed instruction regarding how to make a transgenic animal, which is routine in the art, there is no guidance as to the useful properties of the transgenic animal. Thus, the skilled artisan must resort to experimentation to discover how to use the transgenic animal. The specification provides detailed guidance regarding how one might make and administer a pharmaceutical composition comprising the claimed invention or a pharmaceutical identified using the claimed invention. However, the specification omits critical teachings such as which pharmaceutical composition (*i.e.*, nucleic acid, antibody, agonist or antagonist) should be administered, which patient population should be treated and an effective

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dosage and route of administration. Each of these parameters would have to be established experimentally before any pharmaceutical composition comprising the invention or identified using the invention could be used. Likewise, any diagnostic utility for the claimed invention would have to be established experimentally because the specification fails to teach what, if any, condition could be diagnosed using the invention or diagnostics developed using the claimed invention, and fails to teach what indicators (*i.e.*, increased expression, decreased expression, point mutation, *etc.*) are diagnostic of any condition. Thus, even if a specific and substantial utility can be found in the specification, the disclosure fails to provide a written description of the manner and process of using the invention in such full, clear, concise, and exact terms as to enable the skilled artisan to use the same without undue experimentation.

Relative skill of those in the art and quantity of experimentation needed to make or use the invention: Although the relative level of skill in the art is high, the skilled artisan would not be able to apply the instant invention in a specific “real world” utility without first engaging in undue experimentation. As described above, the art fails to teach any functional properties or any specific or substantial utility for an MA-DBI, and the instant specification provides only broad outlines of potential uses for the claimed invention. Given no more than what is available in the art, the skilled artisan would have to engage in undue empirical experimentation to reasonably establish a substantial research, diagnostic or therapeutic use for the claimed invention or any agent identified using the claimed invention. Therefore, the disclosure fails to enable the claimed subject matter.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

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The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 5-7, 10-14, 39 and 42 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 5, parts (e) and (f) are indefinite. The claims read as follows:

“An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from...(e) a nucleic acid fragment encoding at least a portion of a polypeptide...”, and, “An isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from...(f) a nucleic acid molecule comprising a complement of (a), (b), (c), (d) or (e).”

The claims read as though the nucleic acid molecule encodes a polypeptide comprising an amino acid sequence that is a nucleic acid. Furthermore, a nucleic acid molecule encoding a complement of a nucleic acid encoding a given polypeptide would not itself encode a polypeptide as recited in the preamble. The metes and bounds of the claimed subject matter are unclear because they appear to be inconsistent with the properties of polypeptides and nucleic acids.

Claim 5, part (e) is also indefinite in limiting the nucleic acid to being a fragment without indicating the relative whole. A fragment is generally understood to be a part broken off or detached from a whole. The meaning of the term is therefore unclear unless the “whole” is identified. In other words, it is unclear what distinguishes the nucleic acid fragment of claim 5(e) from any other nucleic acid encoding at least a portion of a polypeptide comprising SEQ ID NO:

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52, especially in light of the fact that a fragment encoding the entirety of SEQ ID NO: 52 is still within the scope of the claim.

Claims 6, 7, 10-14, 39 and 42 are indefinite insofar as they depend from claim 5.

Double Patenting

The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. See *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970); and, *In re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent is shown to be commonly owned with this application. See 37 CFR 1.130(b).

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

Claims 5-14 are provisionally rejected under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims 20-28 of copending Application No. 10/287,971. Although the conflicting claims are not identical, they are not patentably distinct from each other because the claims of the '971 application anticipate the claims of the instant application.

Claims 20-25 of the '971 application are directed to nucleic acids comprising a sequence selected from SEQ ID NO: 2n-1, wherein n is an integer between 1 and 141. When n=139, the claim is directed to a nucleic acid sequence that is 100% identical the instant SEQ ID NO: 51; when n=138, the claim is directed to a sequence that is 99.8% identical to SEQ ID NO: 51; when n=135 or 136, the claim is directed to a sequence that is 99.4% identical to SEQ ID NO: 51; and

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when n=131, the claim is directed to a sequence that is 99.1% identical to SEQ ID NO: 51. The nucleic acids claimed in the '971 application anticipate the nucleic acids encoding SEQ ID NO: 52 and variants and mature forms thereof according to claim 5, 9, 10 and 11, and are naturally occurring according to claims 6 and 7 (see especially the first paragraph on page 4).

Furthermore, the nucleic acid claimed in claim 22 of the '971 application anticipates the nucleic acid differing by a single nucleic acid from SEQ ID NO: 51 according to the instant claim 8; the vector of '971 claims 26 and 27 anticipate the instant claims 12 and 13, respectively; and the cell of '971 claim 28 anticipates the instant claim 14. As the claims of the '971 application anticipate the claims of the instant application, the subject matter claimed in the instant application would be obvious to one of ordinary skill in the art over the claims of the '971 application.

This is a provisional obviousness-type double patenting rejection because the conflicting claims have not in fact been patented.

Claims 5-14 are directed to an invention not patentably distinct from claims 20-28 of application 10/287,971 for the reasons set forth above, which is presumed to be currently commonly assigned. Although the assignment data for the '971 application is not presently available to the examiner, its status as a continuation-in-part of the instant application suggests a common assignee.

The U.S. Patent and Trademark Office normally will not institute an interference between applications or a patent and an application of common ownership (see MPEP § 2302).

Commonly assigned application 10/287,971, discussed above, would form the basis for a rejection of the noted claims under 35 U.S.C. 103(a) if the commonly assigned case qualifies as

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prior art under 35 U.S.C. 102(e), (f) or (g) and the conflicting inventions were not commonly owned at the time the invention in this application was made. In order for the examiner to resolve this issue, the assignee can, under 35 U.S.C. 103(c) and 37 CFR 1.78(c), either show that the conflicting inventions were commonly owned at the time the invention in this application was made, or name the prior inventor of the conflicting subject matter.

A showing that the inventions were commonly owned at the time the invention in this application was made will preclude a rejection under 35 U.S.C. 103(a) based upon the commonly assigned case as a reference under 35 U.S.C. 102(f) or (g), or 35 U.S.C. 102(e) for applications filed on or after November 29, 1999.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Please note, the MPEP 2122 states: “In order to constitute anticipatory prior art, a reference must identically disclose the claimed compound, but *no utility need be disclosed by the reference. In re Schoenwald*, 964 F.2d 1122, 22 USPQ2d 1671 (Fed. Cir. 1992)” (emphasis added). Thus, although the art cited herein below anticipates the claimed nucleic acid, its citation in no way suggests a well-established, enabled utility for the claimed invention.

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Claims 5-7, 9-14, 39 and 42 are rejected under 35 U.S.C. 102(a) as being anticipated by Shimkets *et al.* (12/28/2000) WO 00/78802.

Shimkets *et al.* discloses a nucleic acid comprising a sequence that is 98.6% identical to the instant SEQ ID NO: 51 and encodes a polypeptide that is 98.5% identical to the instant SEQ ID NO: 52 (see the attached sequence alignments with SEC12 (SEQ ID NO: 23) of Shimkets *et al.*). The nucleic acid of Shimkets *et al.* anticipates the nucleic acid encoding a mature form, variant or fragment of the instant SEQ ID NO: 52 according to claims 5, 9, 10 and 11. Furthermore, the nucleic acid of Shimkets *et al.* is naturally occurring according to claim 7 (see especially the final paragraph on page 85) and given the very high degree of similarity (6 mismatches over 1608 nucleotides), absent evidence to the contrary, one of ordinary skill would conclude that the disclosed sequence is an allelic variant according to claim 6. In the section entitled "SECX Recombinant Expression Vectors and Host Cells" beginning on page 42, Shimkets teaches a vector and host cell comprising the disclosed nucleic acid according to claims 12-14, and in the section entitled "Pharmaceutical Compositions" beginning on page 49, Shimkets teaches a pharmaceutical composition and kit comprising a pharmaceutical composition according to claims 39 and 42 (see especially the first full paragraph on page 53).

The nucleic acids, vector, host cell, pharmaceutical composition and kit disclosed by Shimkets *et al.* are the same as those claimed in the instant application. Therefore, the claims are anticipated by Shimkets *et al.*

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Claims 5, 7, 9-12, 14, 39 and 42 are rejected under 35 U.S.C. 102(b) as being anticipated by Webb *et al.* (1987) *DNA* 6:71-79 as evidenced by Sanger *et al.* (1977) *Proc. Natl. Acad. Sci. USA* 74: 5463-5467.

Webb *et al.* discloses a nucleic acid encoding a polypeptide that is 85% identical to the instant SEQ ID NO: 52 (see especially Figure 4 B and the attached sequence alignment). The nucleic acid anticipates the nucleic acid encoding a mature form, variant or portion of SEQ ID NO: 52 according to claim 5, is naturally occurring according to claim 7, anticipates a nucleic acid comprising a fragment of SEQ ID NO: 51 according to claims 9 and would hybridize under “stringent conditions” to SEQ ID NO: 51 according to claim 10.

Claim 11(a) is directed to a nucleic acid molecule which comprises a nucleotide sequence that comprises a coding sequence differing by one or more nucleotide sequences from a coding sequence encoding the amino acid sequence encoded by the nucleic acid of claim 5, wherein no more than 20% of the nucleotides in the sequence differ from said coding sequence. This is understood to encompass any nucleic acid sequence comprising a coding sequence that is at least 80% identical to the coding sequence of any nucleic acid embraced by claim 5, with the proviso that the coding sequence of the claimed nucleic acid must differ from that coding sequence by at least two contiguous nucleotides. The nucleic acid of Webb *et al.*, which encodes a polypeptide that is 85% identical to the instant SEQ ID NO: 52, and would differ from the coding sequence of some nucleic acids within the scope of claim 5 by less than 20% but more than two nucleotides and therefore falls within the scope of the claim 11. The nucleic acid of Webb *et al.* also anticipates the fragment of claim 11(a) and, because the λ gt10 vector used to isolate the

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nucleic acid is double stranded, would comprise the complementary strand according to 11(b) as well.

Finally, Webb *et al.* teaches that the nucleic acid was obtained by screening a λ gt10 library and sequenced by the dideoxy chain-termination method (see especially the left column on page 72). One of ordinary skill in the art would understand that these methods include propagating the nucleic acid comprised within a vector in a host cell and providing the purified nucleic acid in water or a buffer, within a container, suitable for the dideoxy chain-termination reaction (see the second full paragraph on page 5464 of Sanger *et al.*, which was cited by Webb *et al.*). Therefore, the teachings of Webb *et al.* anticipate the vector and host cell of claims 12 and 14. Furthermore, in view of the definition of “pharmaceutically acceptable carrier”, provided in the first paragraph on page 80, as “any and all solvents...compatible with pharmaceutical administration” the nucleic acid comprised within water or buffer inherent to the dideoxy chain-termination method of Webb *et al.* anticipates the pharmaceutical composition and kit of claims 39 and 42.

The nucleic acids, vector, host cell, pharmaceutical composition and kit disclosed by Webb *et al.* are the same as those claimed in the instant application. Therefore, the claims are anticipated by Webb *et al.*

Conclusion

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Daniel M Sullivan whose telephone number is 571-272-0779. The examiner can normally be reached on Monday through Thursday 6:30-5:00.

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If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Remy Yucel, Ph.D. can be reached on 571-272-0781. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

A handwritten signature in black ink, appearing to read 'D. Sullivan', with a stylized flourish at the end.

Daniel M Sullivan, Ph.D.
Examiner
Art Unit 1636

REXRGGETDEFSNVRRGRGRHMOHLSECTKGRQVGSGGDGERWGSDRGSRGSLNEQIA
LVLMLRQEDMQNVLRQKLETLTALQAKSSTLTQTAPQTSQRPSWPFEMSPGVLT
TFAIIWPFIAQWLVLYTORRRKLN"

ORIGIN

Query Match	98.6%;	Score 1597;	DB 6;	Length 2056;
Best Local Similarity	99.6%;	Pred. No. 0;		
Matches 1600;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;
QY	8	CACCATGTTCCAGTTTCATGCAGGCTCTTGGGAAAGCTGTGGTGTGCTGCTGCTGCTGATTC	67	
DB	3	CTCCATGTATNAGTTTCATGCAGGCTCTTGGGAAAGCTGTGGTGTGCTGCTGCTGCTGATTC	62	
QY	68	CGCGGACAGACCTTTGGGACCGGGGCCAACTGTGCAGCTGGAGATGCGGACACGAGATC	127	
DB	63	CGCGGACAGACCTTTGGGACCGGGGCCAACTGTGCAGCTGGAGATGCGGACACGAGATC	122	
QY	128	CGTGCCACACACTAGGTTTTCAGGCGGCGGTGAGGTGATCCAGAGTTTTCGCGAGAGATGG	187	
DB	123	CGTGCCACGACACTAGGTTTTCAGGCGGCGGTGAGGTGATCCAGAGTTTTCGCGAGAGATGA	182	
QY	188	TTCAATTCGACGCCAAACAATGAATGATGCTTAATTTTATAGCTTCTATTAAGCAGGCAAC	247	
DB	183	TTCAATTCGACGCCAAACAATGAATGATGCTTAATTTTATAGCTTCTATTAAGCAGGCAAC	242	
QY	248	TGAAGGACCTGTAAACTTTTCAAGGCTGTGATTTTGGGATCCCTATTGGGAGATATAATG	307	
DB	243	TGAAGGACCTGTAAACTTTTCAAGGCTGTGATTTTGGGATCCCTATTGGGAGATATAATG	302	
QY	308	GGATGCTTGAGTTTCACTGGGTGATATGACCAAGAGAGAACCCATGATTCATATGTTGA	367	
DB	303	GGATGCTTGAGTTTCACTGGGTGATATGACCAAGAGAGAACCCATGATTCATATGTTGA	362	
QY	368	AGAAATGAAAAGATTAATTCGAACCTATGCCCAATGACCTGAGAGGAGTTTGAAGATGCTGG	427	
DB	363	AGAAATGAAAAGATTAATTCGAACCTATGCCCAATGACCTGAGAGGAGTTTGAAGATGCTGG	422	
QY	428	TGTCATAGTGTCATTTTATGAAATTTGCGAGGACAAAAGAGTGCGCAGGAGTTCTGATAT	487	
DB	423	TGTCATAGTGTCATTTTATGAAATTTGCGAGGACAAAAGAGTGCGCAGGAGTTCTGATAT	482	
QY	488	AACCTCAGTCCGACTCGAGAGAAATCTCTAAATGTTTGAAGAGTCTGGTAACTGCTTCAC	547	
DB	483	AACCTCAGTCCGACTCGAGAGAAATCTCTAAATGTTTGAAGAGTCTGGTAACTGCTTCAC	542	
QY	548	TTCTATCTCCGAAACGCCAAAACCGGTTAATGTTAAAGCTGAAAGAGTGACAGTGGAGCCGA	607	
DB	543	TTCTATCTCCAAAACGCCAAAACCGGTTAATGTTAAAGCTGAAAGAGTGACAGTGGAGCCGA	602	
QY	608	GTCTGAGGAGAGAGAGCCCAAGAGAGAGTGAAGAGGACGAGACAAAGTGATATAATGATA	667	
DB	603	GTCTGAGGAGAGAGAGCCCAAGAGAGAGTGAAGAGGACGAGACAAAGTGATATAATGATA	662	
QY	668	GAAATATGATGAAGAGTTCAGAGACCCATATAGAAATTTGGAAAGTCATTGTCTACTAATGGCTA	727	
DB	663	GAAATATGATGAAGAGTTCAGAGACCCATATAGAAATTTGGAAAGTCATTGTCTACTAATGGCTA	722	
QY	728	TGATAAAGATGGCTTTCTTCAGAGATACAGAGATGACATTGACGCCAGTTTCTTCCCTGAA	787	
DB	723	TGATAAAGATGGCTTTCTTCAGAGATACAGAGATGACATTGACGCCAGTTTCTTCCCTGAA	782	
QY	788	TGCGAGAGACACTGAAGAACTAAAGCCCATTTGATGAAAACTTGGGGCAAACTCGAAAAATC	847	
DB	783	TGCGAGAGACACTGAAGAACTAAAGCCCATTTGATGAAAACTTGGGGCAAACTCGAAAAATC	842	
QY	848	TGCTGTTTGCAATTCACCAAGATATAATGATGATCATGTTGGAAGATGTTACAGGAATTC	907	
DB	843	TGCTGTTTGCAATTCACCAAGATATAATGATGATCATGTTGGAAGATGTTACAGGAATTC	902	
QY	908	GCATTTGACAAGGATTCACAGACAGTGAAGTTTACTGTGATTTCTATGAAACAAATTTGGACA	967	
QY	903	GCATTTGACAAGGATTCACAGACAGTGAAGTTTACTGTGATTTCTATGAAACAAATTTGGACA	962	

Qy	968	AGAAGAGTCTTTAGACAGGCTTTACGTC	CAACAAATGGA	CAATTTCA	GTAGTATTA	CTTGGGTGG	1027
Db	963	AGAAGAGTCTTTAGACAGGCTTTACGTC	CAACAAATGGA	CAATTTCA	GTAGTATTA	CTTGGGTGG	1022
Qy	1028	TCATTCAGTCAACCCATGGAAAAATTC	TGGATTTCTGGATTT	CGTGAAGATAT	TTCAAGTACCTCCTGG	1087	
Db	1023	TCATTCAGTCAACCCATGGAAAAATTC	TGGATTTCTGGATTT	CGTGAAGATAT	TTCAAGTACCTCCTGG	1082	
Qy	1088	AAATGCAACANTGGGAAATATCGAGGT	GGTTGTCAGTTG	AGAGAAAGGT	TGAAGTCAAGCA	1147	
Db	1083	AAATGCAACATTTGGGAAATATCGAGGT	GGTTGTCAGTTG	AGAGAAAGGT	TGAAGTCAAGCA	1144	
Qy	1148	TGGAGGAGAAGATGGCAGGAATAACAG	CCGGAGCACCA	CCCGGGAGAAG	CGAGGGGAGA	1207	
Db	1143	TGGAGGAGAAGATGGCAGGAATAACAG	CCGGAGCACCA	CCCGGGAGAAG	CGAGGGGAGA	1202	
Qy	1208	AACGTGACGAATTCCTTAATGTTAGAG	AGGAGAGGACATAG	TGTCACAC	CTTTGAGCA	1267	
Db	1203	AACGTGACGAATTCCTTAATGTTAGAG	AGGAGAGGACATAG	TGTCACAC	CTTTGAGCA	1262	
Qy	1268	AGGAAACAAAGGCGGACAGGTGGGA	TGGAGGTGAT	TGGGAGCGCT	TGGGCTCCGACAG	1327	
Db	1263	AGGAAACAAAGGCGGACAGGTGGGA	TGGAGGTGAT	TGGGAGCGCT	TGGGCTCCGACAG	1322	
Qy	1328	AGGGTCGCGAGGACAGGCTCAATGAG	CAGATCGCCCT	CGTGTGATGAG	ACTGACAGAGGA	1387	
Db	1323	AGGGTCGCGAGGACAGGCTCAATGAG	CAGATCGCCCT	CGTGTGATGAG	ACTGACAGAGGA	1382	
Qy	1388	CATGCGAATATGTCCTTCAGAGACTG	CAGAAA	CTGGAAC	CGCTGAC	1447	
Db	1383	CATGCGAATATGTCCTTCAGAGACTG	CAGAAA	CTGGAAC	CGCTGAC	1442	
Qy	1448	ATCATCAACATCAAACTTGCAGACTG	CTCCTCAG	CGCCACT	CACAGAGACCATCTTGGTG	1507	
Db	1443	ATCATCAACATCAAACTTGCAGACTG	CTCCTCAG	CGCCACT	CACAGAGACCATCTTGGTG	1502	
Qy	1508	GCCCTTCGAGATGTCTCCCTGGTGTC	TACGTTGGCAT	TCATATG	CGCTTTATTCGCA	1567	
Db	1503	GCCCTTCGAGATGTCTCCCTGGTGTC	TACGTTGGCAT	TCATATG	CGCTTTATTCGCA	1562	
Qy	1568	GTGGTTGGTGATTTATATCTATCAAG	AAGAGGAGAA	AACCTCAAC	1613		
Db	1563	GTGGTTGGTGATTTATATCTATCAAG	AAGAGGAGAA	AACCTCAAC	1608		

RESULT 7	REFERENCE
AX133835	AUTHORS
LOCUS	TITLE
DEFINITION	JOURNAL
ACCESSION	FEATURES
VERSION	SOURCE
KEYWORDS	
SOURCE	
ORGANISM	

SDS

AX133835 . 2056 bp DNA linear PAT 15-MAY-2001
Sequence 21 from Patent WO0119856.
AX133835
AX133835.1 GI:14139787
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
Shinkens, R.A., Fernandes, E., Herrmann, J.L., Liu, X., Yang, M. and
Boldog, F.L.
Secreted human proteins, polynucleotides encoding them and methods
of using the same
Patent: WO 0119856-A 21 22-MAR-2001;
Curagen Corporation (US)
Location/Qualifiers
1. .2056
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
7. .1611
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC38968.1"
/db_xref="GI:14139788"

PT New POLYX polypeptide useful for treating or preventing a POLYX
FT associated disorder, e.g. cancer.

PS Claim 9; Page 35-36; 152pp; English.

XX The sequence represents the amino acid sequence of human secreted
CC protein, POLYX. POLYX nucleic acids, polypeptides and antibodies to
CC POLYX can be used for treating or preventing a POLYX associated disorder
CC in a subject, preferably a human. These can be used in the manufacture of
CC a medicament for treating a syndrome associated with a human disease
CC selected from a POLYX-associated disorder, where the therapeutic is a
CC POLYX polypeptide, a POLYX nucleotide or a POLYX antibody. They may also
CC be used to screen for a modulator of activity, or latency, or
CC predisposition to a POLYX associated disorder, e.g. cancer

XX SQ Sequence 534 AA;

Query Match 98.7%; Score 2825; DB 4; Length 534;

Best Local Similarity 99.4%; Pred. No. 4.6e-208;
Matches 531; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

4 MPQFHAGSWESWCCCLIPADRPDGRGQHWOLEMADTRSVHETFEAAVKVQSLPKNQGS 63
1 MYXFHAGSWESWCCCLIPADRPDGRGQHWOLEMADTRSVHETFEAAVKVQSLPKNQGS 60
64 FQPTNEMLKFSFYKQATEGPKLSRPGFWDPIGRYKWDASGLGDMTKEEAMIAVEE 123
61 FQPTNEMLKFSFYKQATEGPKLSRPGFWDPIGRYKWDASGLGDMTKEEAMIAVEE 120
124 MKIITPMTEKVEELLRVIGPFYEIVEDKSGRSSDITSVLEKISKCLEDLGNVLTS 183
121 MKIITPMTEKVEELLRVIGPFYEIVEDKSGRSSDITSVLEKISKCLEDLGNVLTS 180
184 TPNATVNGKAESSDSGAESEEEAEQAEVKGAEOSDNDKMMKKSADHKLELVITNGYD 243
181 TPNATVNGKAESSDSGAESEEEAEQAEVKGAEOSDNDKMMKKSADHKLELVITNGYD 240
244 KGFVQDIONTHASSLNGRSTEVKPIDENLGQTKSAVCIHQDINDHVEDVTGIGH 303
241 KGFVQDIONTHASSLNGRSTEVKPIDENLGQTKSAVCIHQDINDHVEDVTGIGH 300
304 LTSDDSDVYCDSEMFQCEESLDSFTSNNGPFQYLLGHSQPMENSGFREDIQVPPGN 363
301 LTSDDSDVYCDSEMFQCEESLDSFTSNNGPFQYLLGHSQPMENSGFREDIQVPPGN 360
364 GNIGNMQVAVGKGVKHGCGEDGRNNSGAPHREKRGGETDFSNVRGRGHRMQLSEG 423
361 GNIGNMQVAVGKGVKHGCGEDGRNNSGAPHREKRGGETDFSNVRGRGHRMQLSEG 420
424 TKGROVGGSGGERGSGDRGSGSLNEQIALVLMLEQDMQNVLQRLQKLETLTALQAKS 483
421 TKGROVGGSGGERGSGDRGSGSLNEQIALVLMLEQDMQNVLQRLQKLETLTALQAKS 480
484 STSTLTQAPQTSQRPSPWPFEMSPGVLTFAIIPFIAQMLVLYIQRRERKLN 537
481 STSTLTQAPQTSQRPSPWPFEMSPGVLTFAIIPFIAQMLVLYIQRRERKLN 534

RESULT 13

AAB48375
ID AAB48375 standard; protein; 536 AA.

XX AC AAB48375;

XX DT 20-APR-2001 (first entry)

XX DE Human SEC8 protein sequence (clone ID 20936375.0.1).

XX KW SECX; cytostatic; gynecological; gene therapy; screening assay; human;
XX SEC8; chromosomal mapping; forensic biology; cell proliferation; cancer;
XX KW cell differentiation; immune associated disorder; gestational disease.
XX OS Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..15
FT /note= "signal peptide"
FT 16..536
FT Protein /note= "mature protein"

XX WQ200078802-A2.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US017328.

XX 23-JUN-1999; 99US-0140584P.

XX 20-JUL-1999; 99US-0144722P.

XX 16-SEP-1999; 99US-0154520P.

XX 22-JUN-2000; 2000US-00604286.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Fernandes E, Vernet C, Yang M, Boldog FL;
FH Herrmann JL;

XX WPI; 2001-071385/08.

XX N-PSDB; AAC84889.

XX Polynucleotides encoding SECX proteins useful for treating disease
FT characterized by an aberrant level of cell proliferation and/or
FT differentiation like cancer or immune associated disorders.

XX Claim 1; Fig 8; 132pp; English.

XX The invention relates to human SECX polypeptides and polynucleotides
CC encoding them. The SECX polypeptides can be expressed by standard
CC recombinant methodology. The SECX polypeptides are useful for treating or
CC preventing a SECX-associated disorder. The invention is useful in
CC screening assays; detection assays (e.g. chromosomal mapping, cell and
CC tissue typing, forensic biology); predictive medicine (diagnostic assays,
CC prognostic assays, monitoring clinical trials, and pharmacogenomics); and
CC methods of treatment (e.g. therapeutic and prophylactic), especially
CC disorders characterized by aberrant cell proliferation and/or
CC differentiation like cancer or immune associated disorders or gestational
CC disease. The present sequence represents a SEC8 protein

XX SQ Sequence 536 AA;

Query Match 98.5%; Score 2819; DB 4; Length 536;

Best Local Similarity 99.8%; Pred. No. 1.3e-207;

Matches 530; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 FHAGSWESWCCCLIPADRPDGRGQHWOLEMADTRSVHETFEAAVKVQSLPKNQGS 66

Db 6 FHAGSWESWCCCLIPADRPDGRGQHWOLEMADTRSVHETFEAAVKVQSLPKNQGS 65

Qy 67 TNEMLKFSFYKQATEGPKLSRPGFWDPIGRYKWDASGLGDMTKEEAMIAVEEMK 126

Db 66 TNEMLKFSFYKQATEGPKLSRPGFWDPIGRYKWDASGLGDMTKEEAMIAVEEMK 125

Qy 127 ILETNPMTEKVEELLRVIGPFYEIVEDKSGRSSDITSVLEKISKCLEDLGNVLTS 186

Db 126 ILETNPMTEKVEELLRVIGPFYEIVEDKSGRSSDITSVLEKISKCLEDLGNVLTS 185

Qy 187 AKTVNGKAESSDSGAESEEEAEQAEVKGAEOSDNDKMMKKSADHKLELVITNGYD 246

Db 186 AKTVNGKAESSDSGAESEEEAEQAEVKGAEOSDNDKMMKKSADHKLELVITNGYD 245

Qy 247 FVODIONTHASSLNGRSTEVKPIDENLGQTKSAVCIHQDINDHVEDVTGIGH 306

Db 246 FVODIONTHASSLNGRSTEVKPIDENLGQTKSAVCIHQDINDHVEDVTGIGH 305

Qy 307 DSDSEVYCDSEMFQCEESLDSFTSNNGPFQYLLGHSQPMENSGFREDIQVPPGN 366

Db 306 DSDSEVYCDSEMFQCEESLDSFTSNNGPFQYLLGHSQPMENSGFREDIQVPPGN 365

QY 367 GNMQVAVGKGVKGGEDGRNNSGAPRHKRGGETDEFSNVRRGRGHMQLSEGTGK 426
 Db 366 GNMQVAVGKGVKGGEDGRNNSGAPRHKRGGETDEFSNVRRGRGHMQLSEGTGK 425
 QY 427 ROVGGGGERGWSGDRSGSLNECIAIVMLQEDMONTLORLOKLETTALQAKSSTS 486
 Db 426 ROVGGGGERGWSGDRSGSLNECIAIVMLQEDMONTLORLOKLETTALQAKSSTS 485
 QY 487 TLOTAPQTSORPSWPPFEMSPGVLTFAIWPFAQWLVLVLYTQRRRKLN 537
 Db 486 TLOTAPQTSORPSWPPFEMSPGVLTFAIWPFAQWLVLVLYTQRRRKLN 536

RESULT 14

ID ADE28893 standard; protein; 537 AA.

AC ADE28893;

29-JAN-2004 (first entry)

Human NOV261 protein - SEQ ID 270.

NOVX; antidiabetic; anorectic; cardiac; hypotensive;
 antiarteriosclerotic; virucide; antibacterial; fungicide; protozoacide;
 neurotropic; neuroprotective; antiparkinsonian; anticonvulsant;
 osteopathic; antiarthritic; antiinflammatory; dermatological;
 aniaethmatic; antilipemic; metabolic; diabetes; obesity; infectious;
 neurogenic; cancer; cardiovascular; hypertension; atherosclerosis;
 neurodegenerative; Alzheimer's disease; Parkinson's; epilepsy; immune;
 osteoarthritis; haemopoietic; inflammatory skin; asthma; dyslipidaemia;
 neurogenesis; cell differentiation; proliferation; haemopoiesis;
 wound healing; angiogenesis; gene therapy; chromosome mapping;
 tissue typing; human; NOV.

XX Homo sapiens.

OS WO2003040330-A2.

XX 15-MAY-2003.

XX 05-NOV-2002; 2002WO-US035536.

XX 05-NOV-2001; 2001US-0338626P.

XX 05-DEC-2001; 2001US-0336600P.

XX 07-DEC-2001; 2001US-0338285P.

XX 12-DEC-2001; 2001US-0341346P.

XX 17-DEC-2001; 2001US-0341477P.

XX 17-DEC-2001; 2001US-0341540P.

XX 20-DEC-2001; 2001US-0342582P.

XX 27-DEC-2001; 2001US-0344297P.

XX 31-DEC-2001; 2001US-0344903P.

XX 17-APR-2002; 2002US-0373288P.

XX 15-MAY-2002; 2002US-0380981P.

XX 17-MAY-2002; 2002US-0381495P.

XX 28-MAY-2002; 2002US-0383534P.

XX 28-MAY-2002; 2002US-0383744P.

XX 29-MAY-2002; 2002US-0383829P.

XX 29-MAY-2002; 2002US-0384024P.

XX 07-AUG-2002; 2002US-0401788P.

XX 26-AUG-2002; 2002US-0406353P.

XX 31-OCT-2002; 2002US-00287971.

(CURA-) CURAGEN CORP.

XX Alsbrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL;

XX Burgess CB, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;

XX Ellerman X, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;

XX Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV;

XX Lepley DM, Li L, MacDougall JR, Malyankar DM, Mazur A, McQueeney K;

XX Mezes PS, Miller CE, Millet I, Mishra VS, Padigaru M, Patturajan M;

XX Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenozy SG, Shimkets RA;

PI Smithson G, Starling G, Spytek KA, Stone DJ, Tchervnev VT, Twonlow N;
 PI Vernet CAM, Zerhusen BD, Zhong M;
 DR WPI; 2003-441555/41.
 DR N-PSDB; ADE28892.

XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
 PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
 PT asthma, or infections.

XX Claim 1; SEQ ID NO 270; 447pp; English.

XX The invention relates to a novel isolated NOVX polypeptide. The
 CC polypeptide of the invention demonstrates, antidiabetic, anorectic,
 CC cardiac, hypotensive, antiarteriosclerotic, virucide, antibacterial,
 CC fungicide, protozoacide, neurotropic, neuroprotective, antiparkinsonian,
 CC anticonvulsant, osteopathic, antiarthritic, antiinflammatory,
 CC dermatological, antiaethmatic and antilipemic activities. The
 CC polypeptides nucleic acid molecules and antibodies may be useful for
 CC treating or diagnosing diseases including metabolic disorders such as
 CC diabetes and obesity, infectious diseases, anorexia, cancer,
 CC cardiovascular diseases including hypertension and atherosclerosis,
 CC neurodegenerative disorders such as Alzheimer's disease, Parkinson's
 CC disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic
 CC disorders, inflammatory skin disorders, asthma and dyslipidaemia.
 CC Furthermore, the nucleic acids and polypeptides may also be used to
 CC identify molecules that modulate or inhibit neurogenesis, cell
 CC differentiation and proliferation, haemopoiesis, wound healing and
 CC angiogenesis, as well as in gene therapy. Finally, the nucleic acids may
 CC be used as hybridisation probes, in chromosome mapping, tissue typing,
 CC preventive medicine and pharmacogenomics. The current sequence is that of
 CC the human NOV protein of the invention.

XX Sequence 537 AA;

Query Match 98.4%; Score 2818; DB 7; Length 537;

Best Local Similarity 99.1%; Pred. No. 1.6e-207;

Matches 534; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

QY 1 ASTWFOFHAGSWESWCCCCCLIPADRPWDGRQHOLEMADTRSVETRFEEAAVKVQLSPK 60

Db 1 ASTWFOFHAGSWESWCCCCCLIPADRPWDGRQHOLEMADTRSVETRFEEAAVKVQLSPK 60

QY 61 NGSFQPTNEMWLKPYFYKQATEGPKLSRPGFWDPIGRYKWDASLGDMTKEANMAY 120

Db 61 NGSFQPTNEMWLKPYFYKQATEGPKLSRPGFWDPIGRYKWDASLGDMTKEANMAY 120

QY 121 VEEMKKIETMPTEKVEELLRVIGPFYELVEDKSGRSSDITSVLEKISKLEDLGNV 180

Db 121 VEEMKKIETMPTEKVEELLRVIGPFYELVEDKSGRSSDITSVLEKISKLEDLGNV 180

QY 181 LTSTPNKTVNGKAESSDSGAEESEEEAQAEEVKGAGQSDNDKMMKKSADHKLELVITN 240

Db 181 LTSTPN-KTVNGKAESSDSGAEESEEEAQAEEVKGAGQSDNDKMMKKSADHKLELVITN 239

QY 241 GYDQGFVDIIONDIHASSSLNGRSTEEVKPIDENIGOTGKSAVCTHODINDRVEDVTG 300

Db 240 GYDQGFVDIIONDIHASSSLNGRSTEEVKPIDENIGOTGKSAVCTHODINDRVEDVTG 299

QY 301 IOHLTSDSDSEVYCDSEMEQFGQESLDSFTSNNGPFOYILGSHSSQWENSGRPREDIQVP 360

Db 300 IOHLTSDSDSEVYCDSEMEQFGQESLDSFTSNNGPFOYILGSHSSQ-WENSGRPREDIQVP 358

QY 361 PGNGNIGNMQVAVGKGVKGGEDGRNNSGAPRHKRGGETDEFSNVRRGRGHMQL 420

Db 359 PGNGNIGNMQVAVGKGVKGGEDGRNNSGAPRHKRGGETDEFSNVRRGRGHMQL 418

QY 421 SEGTKRGVGGGGERGWSGDRSGSLNECIAIVMLQEDMONTLORLOKLETTALQ 480

Db 419 SEGTKRGVGGGGERGWSGDRSGSLNECIAIVMLQEDMONTLORLOKLETTALQ 478

QY 481 AKSSTSTLOTAPQTSORPSWPPFEMSPGVLTFAIWPFAQWLVLVLYTQRRRKLNLE 539

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OM protein - protein search, using sw model

Run on: July 30, 2004, 09:51:38 ; Search time 14 Seconds
(without alignments)
2004.701 Million cell updates/sec

Title: US-09-997-425-52

Perfect score: 2863

Sequence: 1 ASTMFQFAGSWESWCCCL.....IAQWLVLYYORRRKLNLE 539

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues

total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID
1	2432.5	85.0	533	1 ENDR_BOVIN
2	198.5	6.9	359	1 PECT_HUMAN
3	187	6.5	116	1 YAT7_CABEL
4	178.5	6.2	358	1 PECT_MOUSE
5	176.5	6.2	86	1 ACBP_CHICK
6	174	6.1	89	1 ACBP_GOSHI
7	167.5	5.9	86	1 ACBP_PIG
8	165.5	5.8	86	1 ACBP_HUMAN
9	163.5	5.7	86	1 ACBP_BOVIN
10	162.5	5.7	86	1 ACBP_RABIT
11	162.5	5.7	86	1 ACBP_RAT
12	162	5.7	103	1 ACBP_ANAPL
13	161.5	5.6	86	1 ACBP_MOUSE
14	161.5	5.6	87	1 ACBP_FRIAG
15	161	5.6	90	1 ACBP_RICCO
16	160.5	5.6	86	1 ACBP_CHAVI
17	158.5	5.5	86	1 ACBP_CANFA
18	154	5.4	92	1 ACBP_BRANA
19	149	5.2	92	1 ACBP_ARATH
20	149	5.2	721	1 YC32_ORNPI
21	146.5	5.1	671	1 CHS5_YEAST
22	142	5.0	87	1 ACBP_RANRI
23	142	5.0	5147	1 PCLO_HUMAN
24	141	4.9	622	1 K1C1_HUMAN
25	140.5	4.9	86	1 ACB2_SACPS
26	140.5	4.9	935	1 K1NH_SYNRA
27	140	4.9	730	1 PGL1_CABEL
28	139.5	4.9	937	1 HYR1_CANAL
29	139	4.9	86	1 ACBP_YEAST
30	139	4.9	406	1 NSB1_MOUSE
31	138.5	4.8	4910	1 MDN1_YEAST
32	137	4.8	593	1 SANT_PLAF7
33	136	4.8	5171	1 BPEA_HUMAN

34	134.5	4.7	87	1 DBI5_BOVIN
35	134	4.7	86	1 ACBP_CABEL
36	134	4.7	915	1 NFM_HUMAN
37	132	4.6	1025	1 MK21_YEAST
38	130.5	4.6	2492	1 ATRX_PANTR
39	130.5	4.6	2492	1 ATRX_PONPY
40	129.5	4.5	87	1 DBI5_RAT
41	129	4.5	1130	1 REPT_MOUSE
42	128	4.5	1164	1 BAG_STRAG
43	127.5	4.5	1186	1 CAGA_HELPY
44	127	4.4	416	1 FILA_HUMAN
45	127	4.4	527	1 ATRX_RAT

ALIGNMENTS

RESULT 1
ENDR_BOVIN STANDARD; PRT; 533 AA.
AC P07106;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Endoepine-related protein precursor (Membrane-associated diazepam
DE Binding inhibitor) (MA-DBI).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_TaxID=9913;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87161236; PubMed=2881742;
RA Webb N.R., Rose T.M., Malik N., Marquardt H., Shoyab M., Todaro G.J.,
RA Lee D.C.;
RT "Bovine and human cDNA sequences encoding a putative benzodiazepine
RT receptor ligand";
RL DNA 6:71-79(1987).
[2]
RN SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=92140578; PubMed=1780036;
RA Todaro G.J., Rose T.M., Shoyab M.;
RT "Human DBI (endoepine): relationship to a homologous membrane
RT associated protein (MA-DBI).";
RL Neuropharmacology 30:1373-1380(1991).
CC -!- TISSUE SPECIFICITY: Highly expressed in brain and liver. Lower
CC levels of expression in spleen and heart.
CC -!- SIMILARITY: In the N-terminal section; belongs to the ACBP family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M15888; AAA30496.1; -;
CC EMBL; S80107; AAB21311.2; -;
CC PIR; C26448; NZBOR.
CC
CC InterPro: IPR000582; Ac_coa_bind_prot.
CC HSP; P07107; IACA.
CC Pfam; PF00887; ACBP; 1.
CC PRINTS; PR00689; AC0ABINDINGP.
CC ProDom; PD351532; AC_coa_bind_prot; 1.
CC PROSITE; PS00880; ACBP; 1.
CC Signal; Transmembrane; Glycoprotein; Transport; Lipid-binding.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 533 ENDOEPINE-RELATED PROTEIN.
FT DOMAIN 41 139 ACBP

FT	TRANSMEM	502	526	POTENTIAL
FT	CARBOHYD	59	59	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	341	341	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	361	361	N-LINKED (GLCNAC. . .) (POTENTIAL) .
SEQ	SEQUENCE	533 AA;	59759 MW;	B2A396895214B0EE CRC64;

Query Match	85.0%;	Score 2432.5;	DB 1;	Length 533;
Best Local Similarity	85.2%;	Prod. No. 5.1e-131;		
Matches 456;	Conservative	47;	Indels 3;	Gaps 2;

QY	4	MFOFHAGSWESW - CCCCLIPADRPWDRCQHWQEMADTSVHETREFAAVKVQTSIPQIG 62
Db	1	MFOFHAGSWESWCCCCCLIPGDRPWRGRWRLEWHTTSVTEFPFAAVKVQTSIPQIG 60
QY	63	SFOPTNEMMLKPYFYKATGEGCKLGRPFQWDPGRYKWDANSLSGDMTKEEMIAVYE 122
Db	61	SFOPTNEMMLKPYFYKATGEGCKLSKSGFNDPGRYKWDANSLSGDMTKEEMIAVYE 120
QY	123	EMKKTIEIMPMTXKVEBLLRVIQFPFVEYEDKSGRSSDITSVRLEKISKLEDLGNVLT 182
Db	121	EMKKTIEIMPMTXKVEBLLRVIQFPFVEYEDKSGRSSDLTSVRLEKISKLEDLGNVLA 180
QY	183	STPNAKTVNGKAESSDSGAESSEERAEQVEYKGAQSQNDKGMKKYASDHQNLVITNGY 242
Db	181	STPNAKTVNGKAESSDSGAESSEERAAQDPKPPRSDKGMKKYASDHQNLVITNGY 240
QY	243	DKDGFVQIQNDIHAASSLNGRSTBEVYKIDENLACTKSAVCHODINDHDVDTGIG 302
Db	241	DKDGFVQVQNSIHTSPSLNGRCSTEEVKSVDENLEQTKTVFVHQVDNSHDVDTSGIG 300
QY	303	HLTSDSDSEYVCDSMEQFOCESLOSFTSNNGPPQYTVIGHSSQPMENSGFPREDIQVPPG 362
Db	301	HLTSDSDSEYVCDSMEQFOCESLDCFTSNNGPFYVYVGNPFSQPLESSGPFPAVQGLPG 360
QY	363	NGNIGNQWVVAVEGKGEVKHGQEDGRNNSGAPAREKRGCGTDEFSNVRGRGRHMOHLE 422
Db	361	NGSPEDMQAVVEGKGEVKHGQEDGCSNGSAPAREKRGAGESEESFNIRGRGRHMOHLE 420
QY	423	GTKGHQVSGGDEGRKWSDRSGSGLNEQIALVLMRLQEDMNQVLRQKLSTLTALQAK 482
Db	421	GSKGRQVSGGDEGRWGSORGSRGSLNQCIALVLMRLQEDMNQVLRQKLHUEMLAASQAK 480
QY	483	SSTSTLTQATQPQTSQRPSWWPEMSPGVLTFTAIWPFIAQNLVYIYQRRERKLN 537
Db	481	S-SALQTSNQPTSPRPSWWPEMSPGALTFTAIWPFIAQNLVYIYQRRERKLN 533

RESULT 2

PREC JMAN STANDARD: PRT; 359 AA.
 AC J75521; Q9BU9; Q9NH1; Q9NH7; Q9UN55;
 DT 15-JUN-1999 (Rel. 38, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DT Peroxisomal 3,2-trans-enoyl-CoA isomerase (EC 5.3.3.8) (Dodeceno-yl-CoA
 DE delta-isomerase) (D3,D2-eno-yl-CoA isomerase) (DBI-related protein 1)
 DE (DRS-1) (Hepatocellular carcinoma-associated antigen 88).
 EN PEI OR DRS1 OR HCA48.
 EN Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCB1_TaxID=9606;
 [1]
 EN SEQUENCE FROM N.A.
 IP TISSUE=Pancratic islets;
 IC MEDLINE=99284489; PubMed=10354522;
 IC Suk K., Kim Y.-H., Hwang D.-Y., Ihm S.-H., Yoo H.J., Lee M.-S.;
 IC "Molecular cloning and expression of a novel human cDNA related to the
 IC diazepam binding inhibitor";
 IC Biochim. Biophys. Acta 1454:126-131 (1999).
 [2]
 EN SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.
 IC MEDLINE=99348312; PubMed=10419495;

[illegible]